



SEQUENCE LISTING

<110> ASAKO, HIROYUKI
MATSUMURA, KENJI
SHIMIZU, MASATOSHI
ITO, NOBUYA
WAKITA, RYUHEI

<120> PROCESS FOR PRODUCING OPTICALLY ACTIVE
4-HALO-3-HYDROXYBUTANOATE

<130> 7372-72249

<140> 10/004,115
<141> 2001-12-06

<150> JP 2000-372704
<151> 2000-12-07

<150> JP 2001-006144
<151> 2001-01-15

<150> JP 2001-026594
<151> 2001-02-02

<150> JP 2001-175175
<151> 2001-06-11

<160> 37

<170> PatentIn Ver. 2.1

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Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr
20 25 30

Tyr Thr Ala Val Thr Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp
35 40 45

Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg
50 55 60

Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val
65 70 75 80

Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp
85 90 95

Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met
100 105 110

Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu
 115 120 125
 Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr
 130 135 140
 Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp
 145 150 155 160
 Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu
 165 170 175
 Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile
 180 185 190
 Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe
 195 200 205
 Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn
 210 215 220
 Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn
 225 230 235 240
 Glu Ile Ala Glu Lys Gly Asn Thr Leu Ala Gln Val Leu Ile Ala
 245 250 255
 Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro
 260 265 270
 Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp
 275 280 285
 Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val
 290 295 300
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 305 310 315 320
 Lys Asn Leu Ser Ala
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<210> 2
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ggc gtc ggc ttt ggt acc ttc gct agt gaa ggt tcc aag ggc gag acc	96
Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr	
20 25 30	
tat act gct gtc acc act gcc ctg aag acc ggt tac cgt cac ttg gac	144
Tyr Thr Ala Val Thr Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp	
35 40 45	
tgt gcc tgg tac tac ctg aac gag ggt gag gtt ggt gag ggt atc cgt	192
Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg	
50 55 60	
gac ttc ctg aag gag aac ccc tcg gtg aag cgt gag gac atc ttc gtc	240
Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val	
65 70 75 80	
tgc acc aag gtg tgg aac cac ctc cac cgt tat gag gac gtc ctc tgg	288
Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp	
85 90 95	
tcc att gac gac tcc ctg aag cgt ctt gga ctt gac tac gtt gat atg	336
Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met	
100 105 110	
ttc ctc gtt cac tgg ccc att gct gcc gag aag aat ggc cag ggt gag	384
Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu	
115 120 125	
ccc aag att ggc cct gac ggc aaa tac gtc att ctc aag gac ctg acc	432
Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr	
130 135 140	
gag aac ccc gag ccc aca tgg cgc gct atg gag aag att tat gag gat	480
Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp	
145 150 155 160	
cgc aag gcc agg tcc att ggt gtc tcc aac tgg acc att gcc gac ctt	528
Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu	
165 170 175	
gag aag atg tcc aag ttc gcc aag gtc atg cct cac gcc aac cag atc	576
Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile	
180 185 190	
gag att cac ccc ttc ctg ccc aac gag gag ctg gtg cag tac tgc ttc	624
Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe	
195 200 205	
tcc aag aac att atg ccc gtg gcc tac tct cct ctg ggc tcg cag aac	672
Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn	
210 215 220	
cag gtt ccc acc acc ggt gag cggt gtc agc gag aac aag act ctg aac	720
Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn	
225 230 235 240	

gag atc gcc gag aag ggc ggc aac acc ctt gct cag gtt ctt att gcc	768		
Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala			
245	250	255	
tgg ggt ctg cgc cgt ggc tac gtc gtt ctc ccc aag agc tcc aac ccc	816		
Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro			
260	265	270	
aag cgc att gag tcc aac ttc aag agc att gag ctc tcc gat gcc gac	864		
Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp			
275	280	285	
ttt gaa gcc atc aat gcc gtt gcc aag ggt cgt cac ttc cgt ttc gtc	912		
Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val			
290	295	300	
aac atg aag gat act ttc gga tat gat gtc tgg ccc gag gag acc gcc	960		
Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala			
305	310	315	320
aag aac ctg tct gcg tga	978		
Lys Asn Leu Ser Ala			
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<212> PRT

<213> Penicillium citrinum

<400> 3

Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn Gln Val			
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Pro

<210> 4

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<212> PRT

<213> Penicillium citrinum

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<211> 14

<212> PRT

<213> Penicillium citrinum

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<210> 7

<400> 7
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<210> 8
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 8
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<210> 9
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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<220>
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<210> 14
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<220>
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aanacttca cactgagcaa cggcgtaaa attcctggcg tcggctttgg tacctncgt 120
agtgaaggtt ccaagggcga aacatatnct gctgtcacca ctgccctgaa aaccggttac 180
cgtncttg actgtgcctg gtactacctg aacaagggtg aggttggtga gggtnccgt 240
gacttcctga agaaaaaccc ctcggtaag cgtgaggaca tttcgatctg caccaaggta 300
tggaaaccacc tccaccgtta tgaggacgtc ctctggtcca ttgacnactc cctgaagcgt 360
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cttggacttg actacgttga tatgttcctc gttcaactggc ccattgctgc cgaaaaaaaaat 420
 ggccagggtg agccccaaat tggccctgac ggcaaatacn tcnttctcaa ggacctgacc 480
 gaaanccna ncccacctgg cgcgctatgg aaaaaatttn tgangatccc aaggccaggt 540
 ccattggtgt ttccaattgg accattgccc accttgagaa gatgtccaag ttngccaagg 600
 tnatgcctca cgccaaaccag atcgagattc accccttcct gcccaacgag gagctggtgc 660
 agtactgctt ttccaagaac antatgcccg tagcgta 697

<210> 16
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 16
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<210> 17
 <211> 20
 <212> DNA
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<220>
 <223> Description of Artificial Sequence: Primer

<400> 17
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<210> 18
 <211> 331
 <212> DNA
 <213> Escherichia coli

<220>
 <221> modified_base
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 cccatcatgt ctaacggaaa gactttcaca tttagtgcacg gcgtcaagat tcctggcgtc 120
 ggctttggta ccttcgttag tgaagggtcc aaggggcgaga cctataactgc tgtcaccact 180
 gcccctgaaga ccgttaccg tcacttggac tttgcctgggt actacctgaa cgagggtgag 240
 gttggtgagg gtatccgtga cttcctgaag gagaacccct cggtgaagcg tgaggacatc 300
 ttctgtctgca ccaagggtgtc gaaccacctc c 331

<210> 19
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cggtgagcgg gtcagcgaga acaagactct gaacgagatc gccgagaagg gcggcaacac 180
ccttgctcag gttcttattg cctggggctc gcccgtggc tacgtcgatc tccccaaagag 240
ctccaacccc aagcgcatgg agtccaactt caagagcatg gagctctccg atgccgactt 300
tgaagccatc aatgccgttg ccaagggtcg tcacttccgt ttcgtcaaca tgaaggatac 360
tttcggatat gatgtctggc ccgaggagac cgccaaagaac ctgtctgcgt gaatctctac 420
gaaaattataa aatnacaccc acnaaaaanc aaagcganag gatgatnccc aaaantttg 480
agggtttctt ggtgaaaaac gtttattgan cccgaantga angaataagat gancttgatt 540
tctccaaaaa aaaaaaaaaa aaaaacggtc cgcggccgtt ccnnnggggg gcccgggttcc 600
caattcnccc cttatnattt aattctttt taanggggncc aaattccncc nnattccnt 660
cnaatttgn nggccgcctc caaactttcn tcntnaaagg gncccaattc ccccccnatt 720
aantggantt cctntttacc ttt 743

<210> 20
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 20
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<210> 21
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 21
ccagaggaga gtaggccacg g 21

<210> 22
<211> 417
<212> DNA
<213> Escherichia coli

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agaagaatgg ccagggtgag cccaaaggattt ggcctgacgg caaatacgtc attctcaagg 180
acctgaccga gaacccccgag cccacatggc ggcgttatggta gaagattttt gaggatcgca 240
aggccagggc cattgggtgtc tccaactggta ccattggccga ccttgagaag atgtccaagt 300
tcgccaaggat catggcctcac gccaaccaga tcgagattca ccccttcctg cccaaacgagg 360
agctggtgca gtactgcttc tccaagaaca ttatggccgt ggcctactct cctctgg 417

<210> 23
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 23
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<210> 24
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<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Primer

<400> 24
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<210> 25
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

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<210> 26
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<212> DNA
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<220>
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<210> 27
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<212> DNA
<213> Escherichia coli

<220>
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<222> (1)..(783)

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   1           5           10          15
                                         15

acc ggt tta gga aaa gca atg gcg att cgt ttt gcg aca gaa aaa gct    96
Thr Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Ala Thr Glu Lys Ala
   20          25          30
                                         30

aaa gta gtt gtg aac tat cgt tcg aaa gaa gaa gaa gct aac aac gtt    144
Lys Val Val Asn Tyr Arg Ser Lys Glu Glu Ala Asn Ser Val
   35          40          45
                                         45

tta gaa gaa att aaa aaa gtg ggc gga gag gct att gcc gtc aaa ggt    192
Leu Glu Glu Ile Lys Lys Val Gly Gly Glu Ala Ile Ala Val Lys Gly
   50          55          60
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gat gta aca gtt gag tct gat gtg atc aat tta gtt caa tct gct att		240
Asp Val Thr Val Glu Ser Asp Val Ile Asn Leu Val Gln Ser Ala Ile		
65 70 75 80		
aaa gaa ttt gga aag cta gac gtt atg att aat aac gca gga atg gaa		288
Lys Glu Phe Gly Lys Leu Asp Val Met Ile Asn Asn Ala Gly Met Glu		
85 90 95		
aat ccg gtt tcg tct cat gaa atg tct tta agt gat tgg aat aaa gtc		336
Asn Pro Val Ser Ser His Glu Met Ser Leu Ser Asp Trp Asn Lys Val		
100 105 110		
att gat acg aac tta acg gga gca ttt tta ggc agc cgt gaa gcg att		384
Ile Asp Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile		
115 120 125		
aaa tat ttt gtg gaa aat gat att aag gga aca gtt att aac atg tcg		432
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Thr Val Ile Asn Met Ser		
130 135 140		
agt gtt cac gag aaa att cct tgg cca tta ttt gtt cat tac gca gca		480
Ser Val His Glu Lys Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala		
145 150 155 160		
agt aaa ggc gga atg aag ctc atg acc gaa aca ctt gca tta gaa tac		528
Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr		
165 170 175		
gct cca aaa ggt att cgt gta aat aac att gga ccg gga gcg att aat		576
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn		
180 185 190		
aca ccg att aac gct gag aaa ttt gct gat cct gag cag cgt gca gat		624
Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Glu Gln Arg Ala Asp		
195 200 205		
gta gaa agc atg att cca atg gga tac att gga gag ccg gaa gaa att		672
Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile		
210 215 220		
gca gcg gtt gct gca tgg cta gct tct tca gag gca agt tat gta aca		720
Ala Ala Val Ala Ala Trp Leu Ala Ser Ser Glu Ala Ser Tyr Val Thr		
225 230 235 240		
ggg att aca ctc ttt gct gac ggc ggt atg aca cag tac cca tca ttc		768
Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe		
245 250 255		
caa gca gga cgc gga taa		786
Gln Ala Gly Arg Gly		
260		

<210> 28

<211> 996

<212> DNA

<213> Penicillium citrinum

<220>
 <221> CDS
 <222> (1)..(975)

<400> 28

atg tct aac gga aag act ttc aca ttg agc aac ggc gtc aag att cct	48
Met Ser Asn Gly Lys Thr Phe Thr Leu Ser Asn Gly Val Lys Ile Pro	
1 5 10 15	

ggc gtc ggc ttt ggt acc ttc gct agt gaa ggt tcc aag ggc gag acc

Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr	96
20 25 30	

tat act gct gtc acc act gcc ctg aag acc ggt tac cgt cac ttg gac

Tyr Thr Ala Val Thr Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp	144
35 40 45	

tgt gcc tgg tac tac ctg aac gag ggt gag gtt ggt gag ggt atc cgt

Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg	192
50 55 60	

gac ttc ctg aag gag aac ccc tcg gtg aag cgt gag gac atc ttc gtc

Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val	240
65 70 75 80	

tgc acc aag gtg tgg aac cac ctc cac cgt tat gag gac gtc ctc tgg

Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp	288
85 90 95	

tcc att gac gac tcc ctg aag cgt ctt gga ctt gac tac gtt gat atg

Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met	336
100 105 110	

ttc ctc gtt cac tgg ccc att gct gcc gag aag aat ggc cag ggt gag

Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu	384
115 120 125	

ccc aag att ggc cct gac ggc aaa tac gtc att ctc aag gac ctg acc

Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr	432
130 135 140	

gag aac ccc gag ccc aca tgg cgc gct atg gag aag att tat gag gat

Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp	480
145 150 155 160	

cgc aag gcc agg tcc att ggt gtc tcc aac tgg acc att gcc gac ctt

Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu	528
165 170 175	

gag aag atg tcc aag ttc gcc aag gtc atg cct cac gcc aac cag atc

Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile	576
180 185 190	

gag att cac ccc ttc ctg ccc aac gag gag ctg gtg cag tac tgc ttc

Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe	624
195 200 205	

tcc aag aac att atg ccc gtg gcc tac tct cct ctg ggc tcg cag aac Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn 210 215 220	672
cag gtt ccc acc acc ggt gag cggt gtc agc gag aac aag act ctg aac Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn 225 230 235 240	720
gag atc gcc gag aag ggc ggc aac acc ctt gct cag gtt ctt att gcc Glu Ile Ala Glu Lys Gly Asn Thr Leu Ala Gln Val Leu Ile Ala 245 250 255	768
tgg ggt ctg cgc cgt ggc tac gtc gtt ctc ccc aag agc tcc aac ccc Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro 260 265 270	816
aag cgc att gag tcc aac ttc aag agc att gag ctc tcc gat gcc gac Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp 275 280 285	864
ttt gaa gcc atc aat gcc gtt gcc aag ggt cgt cac ttc cgt ttc gtc Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val 290 295 300	912
aac atg aag gat act ttc gga tat gat gtc tgg ccc gag gag acc gcc Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala 305 310 315 320	960
aag aac ctg tct gcg tgaatctcta cgaaaattata a Lys Asn Leu Ser Ala 325	996

<210> 29

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 29

cgatatccgtt cacgcagaca ggttcttgg

29

<210> 30

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 30

gccatggcta tgtataaaga ttttagaa

27

<210> 31

<400> 31
000

<210> 32
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 32
cgatatccgtt atccgcgtcc tgc

23

<210> 33
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 33
cgatatccgag cgcccaatac gcaaaccg

28

<210> 34
<211> 385
<212> PRT
<213> Corynebacterium sp.

<400> 34
Met Lys Ala Ile Gln Tyr Thr Arg Ile Gly Ala Glu Pro Glu Leu Thr
1 5 10 15

Glu Ile Pro Lys Pro Glu Pro Gly Pro Gly Glu Val Leu Leu Glu Val
20 25 30

Thr Ala Ala Gly Val Cys His Ser Asp Asp Phe Ile Met Ser Leu Pro
35 40 45

Glu Glu Gln Tyr Thr Tyr Gly Leu Pro Leu Thr Leu Gly His Glu Gly
50 55 60

Ala Gly Lys Val Ala Ala Val Gly Glu Gly Val Glu Gly Leu Asp Ile
65 70 75 80

Gly Thr Asn Val Val Val Tyr Gly Pro Trp Gly Cys Gly Asn Cys Trp
85 90 95

His Cys Ser Gln Gly Leu Glu Asn Tyr Cys Ser Arg Ala Gln Glu Leu
100 105 110

Gly Ile Asn Pro Pro Gly Leu Gly Ala Pro Gly Ala Leu Ala Glu Phe
 115 120 125

Met Ile Val Asp Ser Pro Arg His Leu Val Pro Ile Gly Asp Leu Asp
 130 135 140

Pro Val Lys Thr Val Pro Leu Thr Asp Ala Gly Leu Thr Pro Tyr His
 145 150 155 160

Ala Ile Lys Arg Ser Leu Pro Lys Leu Arg Gly Gly Ser Tyr Ala Val
 165 170 175

Val Ile Gly Thr Gly Gly Leu Gly His Val Ala Ile Gln Leu Leu Arg
 180 185 190

His Leu Ser Ala Ala Thr Val Ile Ala Leu Asp Val Ser Ala Asp Lys
 195 200 205

Leu Glu Leu Ala Thr Lys Val Gly Ala His Glu Val Val Leu Ser Asp
 210 215 220

Lys Asp Ala Ala Glu Asn Val Arg Lys Ile Thr Gly Ser Gln Gly Ala
 225 230 235 240

Ala Leu Val Leu Asp Phe Val Gly Tyr Gln Pro Thr Ile Asp Thr Ala
 245 250 255

Met Ala Val Ala Gly Val Gly Ser Asp Val Thr Ile Val Gly Ile Gly
 260 265 270

Asp Gly Gln Ala His Ala Lys Val Gly Phe Phe Gln Ser Pro Tyr Glu
 275 280 285

Ala Ser Val Thr Val Pro Tyr Trp Gly Ala Arg Asn Glu Leu Ile Glu
 290 295 300

Leu Ile Asp Leu Ala His Ala Gly Ile Phe Asp Ile Gly Gly Asp
 305 310 315 320

Leu Gln Ser Arg Gln Arg Cys Arg Ser Val Ser Thr Thr Gly Cys Arg
 325 330 335

Asn Ala Gln Arg Pro Cys Gly Cys Gly Pro Trp Ser Val Val Pro Thr
 340 345 350

Ala Val Glu Arg Gln Arg Lys Asn Thr Asp Ala Arg Pro Asn Ser Ile
 355 360 365

Arg Pro Gly Ile Ser Val Arg Asn Ser Val Cys Ala Ser Cys Thr Pro
 370 375 380

Arg
385

<210> 35
<211> 1158

<212> DNA

<213> Corynebacterium sp.

<220>

<221> CDS

<222> (1)..(1155)

<400> 35

atg aag gcg atc cag tac acg cga atc ggc gcg gaa ccc gaa ctc acg	48
Met Lys Ala Ile Gln Tyr Thr Arg Ile Gly Ala Glu Pro Glu Leu Thr	
1 5 10 15	

gag att ccc aaa ccc gag ccc ggt cca ggt gaa gtg ctc ctg gaa gtc	96
Glu Ile Pro Lys Pro Glu Pro Gly Pro Gly Glu Val Leu Leu Glu Val	
20 25 30	

acc gct gct ggc gtc tgc cac tcg gac gac ttc atc atg agc ctg ccc	144
Thr Ala Ala Gly Val Cys His Ser Asp Asp Phe Ile Met Ser Leu Pro	
35 40 45	

gaa gag cag tac acc tac ggc ctt ccg ctc acg ctc ggc cac gaa ggc	192
Glu Glu Gln Tyr Thr Tyr Gly Leu Pro Leu Thr Leu Gly His Glu Gly	
50 55 60	

gca ggc aag gtc gcc gcc gtc ggc gag ggt gtc gaa ggt ctc gac atc	240
Ala Gly Lys Val Ala Val Gly Glu Gly Val Glu Gly Leu Asp Ile	
65 70 75 80	

gga acc aat gtc gtc tac ggg cct tgg ggt tgc ggc aac tgt tgg	288
Gly Thr Asn Val Val Tyr Gly Pro Trp Gly Cys Gly Asn Cys Trp	
85 90 95	

cac tgc tca caa gga ctc gag aac tat tgc tct cgc gcc caa gaa ctc	336
His Cys Ser Gln Gly Leu Asn Tyr Cys Ser Arg Ala Gln Glu Leu	
100 105 110	

gga atc aat cct ccc ggt ctc ggt gca ccc ggc gcg ttg gcc gag ttc	384
Gly Ile Asn Pro Pro Gly Leu Ala Pro Gly Ala Leu Ala Glu Phe	
115 120 125	

atg atc gtc gat tct cct cgc cac ctt gtc ccg atc ggt gac ctc gac	432
Met Ile Val Asp Ser Pro Arg His Leu Val Pro Ile Gly Asp Leu Asp	
130 135 140	

ccg gtc aag acg gtg ccg ctg acc gac gcc ggt ctg acg ccg tat cac	480
Pro Val Lys Thr Val Pro Leu Thr Asp Ala Gly Leu Thr Pro Tyr His	
145 150 155 160	

gcg atc aag cgt tct ctg ccg aaa ctt cgc gga ggc tcg tac gcg gtt	528
Ala Ile Lys Arg Ser Leu Pro Lys Leu Arg Gly Ser Tyr Ala Val	
165 170 175	

gtc att ggt acc ggc ggt ctc ggc cac gtc gct att cag ctc ctc cgc	576
Val Ile Gly Thr Gly Leu Gly His Val Ala Ile Gln Leu Leu Arg	
180 185 190	

cac ctc tcg gcg gca acg gtc atc gct ttg gac gtg agc gcg gac aag	624
His Leu Ser Ala Ala Thr Val Ile Ala Leu Asp Val Ser Ala Asp Lys	
195 200 205	
ctc gaa ctg gca acc aag gta ggc gct cac gaa gtg gtt ctg tcc gac	672
Leu Glu Leu Ala Thr Lys Val Gly Ala His Glu Val Val Leu Ser Asp	
210 215 220	
aag gac gcg gcc gag aac gtc cgc aag atc act gga agt caa ggc gcc	720
Lys Asp Ala Ala Glu Asn Val Arg Lys Ile Thr Gly Ser Gln Gly Ala	
225 230 235 240	
gca ttg gtt ctc gac ttc gtc ggc tac cag ccc acc atc gac acc gcg	768
Ala Leu Val Leu Asp Phe Val Gly Tyr Gln Pro Thr Ile Asp Thr Ala	
245 250 255	
atg gct gtc gcc ggc gtc gga tca gac gtc acg atc gtc ggg atc ggg	816
Met Ala Val Ala Gly Val Gly Ser Asp Val Thr Ile Val Gly Ile Gly	
260 265 270	
gac ggc cag gcc cac gcc aaa gtc ggg ttc ttc caa agt cct tac gag	864
Asp Gly Gln Ala His Ala Lys Val Gly Phe Phe Gln Ser Pro Tyr Glu	
275 280 285	
gct tcg gtg aca gtt ccg tat tgg ggt gcc cgc aac gag ttg atc gaa	912
Ala Ser Val Thr Val Pro Tyr Trp Gly Ala Arg Asn Glu Leu Ile Glu	
290 295 300	
ttg atc gac ctc gcc cac gcc ggc atc ttc gac atc ggc ggt gga gac	960
Leu Ile Asp Leu Ala His Ala Gly Ile Phe Asp Ile Gly Gly Asp	
305 310 315 320	
ctt cag tct cga caa cgg tgc cga agc gta tcg acg act ggc tgc cgg	1008
Leu Gln Ser Arg Gln Arg Cys Arg Ser Val Ser Thr Thr Gly Cys Arg	
325 330 335	
aac gct cag cgg cgc tgc ggt tgt ggt ccc tgg tct gta gta ccc aca	1056
Asn Ala Gln Arg Pro Cys Gly Cys Gly Pro Trp Ser Val Val Pro Thr	
340 345 350	
gcg gta gaa cga cag cgg aaa aac act gat gcc cgg ccc aat tcg att	1104
Ala Val Glu Arg Gln Arg Lys Asn Thr Asp Ala Arg Pro Asn Ser Ile	
355 360 365	
cgg ccc ggc atc agt gtc aga aat tcg gtg tgc gct agc tgc acg cct	1152
Arg Pro Gly Ile Ser Val Arg Asn Ser Val Cys Ala Ser Cys Thr Pro	
370 375 380	
cga tga	1158
Arg	
385	

<210> 36
<211> 261
<212> PRT
<213> Escherichia coli

<400> 36

Met	Tyr	Lys	Asp	Leu	Glu	Gly	Lys	Val	Val	Val	Ile	Thr	Gly	Ser	Ser
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Thr	Gly	Leu	Gly	Lys	Ala	Met	Ala	Ile	Arg	Phe	Ala	Thr	Glu	Lys	Ala
				20				25				30			

Lys	Val	Val	Val	Asn	Tyr	Arg	Ser	Lys	Glu	Glu	Glu	Ala	Asn	Ser	Val
				35			40				45				

Leu	Glu	Glu	Ile	Lys	Lys	Val	Gly	Gly	Glu	Ala	Ile	Ala	Val	Lys	Gly
				50		55			60						

Asp	Val	Thr	Val	Glu	Ser	Asp	Val	Ile	Asn	Leu	Val	Gln	Ser	Ala	Ile
65				70				75			80				

Lys	Glu	Phe	Gly	Lys	Leu	Asp	Val	Met	Ile	Asn	Asn	Ala	Gly	Met	Glu
				85			90				95				

Asn	Pro	Val	Ser	Ser	His	Glu	Met	Ser	Leu	Ser	Asp	Trp	Asn	Lys	Val
				100			105				110				

Ile	Asp	Thr	Asn	Leu	Thr	Gly	Ala	Phe	Leu	Gly	Ser	Arg	Glu	Ala	Ile
				115			120				125				

Lys	Tyr	Phe	Val	Glu	Asn	Asp	Ile	Lys	Gly	Thr	Val	Ile	Asn	Met	Ser
				130			135			140					

Ser	Val	His	Glu	Lys	Ile	Pro	Trp	Pro	Leu	Phe	Val	His	Tyr	Ala	Ala
145				150				155			160				

Ser	Lys	Gly	Gly	Met	Lys	Leu	Met	Thr	Glu	Thr	Leu	Ala	Leu	Glu	Tyr
				165			170			175					

Ala	Pro	Lys	Gly	Ile	Arg	Val	Asn	Asn	Ile	Gly	Pro	Gly	Ala	Ile	Asn
				180			185			190					

Thr	Pro	Ile	Asn	Ala	Glu	Lys	Phe	Ala	Asp	Pro	Glu	Gln	Arg	Ala	Asp
				195			200			205					

Val	Glu	Ser	Met	Ile	Pro	Met	Gly	Tyr	Ile	Gly	Glu	Pro	Glu	Glu	Ile
				210			215			220					

Ala	Ala	Val	Ala	Ala	Trp	Leu	Ala	Ser	Ser	Glu	Ala	Ser	Tyr	Val	Thr
225				230				235			240				

Gly	Ile	Thr	Leu	Phe	Ala	Asp	Gly	Gly	Met	Thr	Gln	Tyr	Pro	Ser	Phe
				245			250			255					

Gln	Ala	Gly	Arg	Gly											
				260											

<210> 37

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 37

Trp Ile Ser Thr Lys Leu
1 5